L Number	Hits	Search Text	DB	Time stamp
-	685	Goldberg NEAR Edward	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/12/09 14:01
-	5	(Goldberg NEAR Edward) and phage	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/12/09 14:03
-	23544	bacteriophage	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/12/09 14:04
-	7223	bacteriophage and tail	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/12/09 14:04
-	6	(bacteriophage and tail) and gp35	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/12/09 14:06
-	5	(Goldberg NEAR Edward) and bacteriophage	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/12/09 14:07
-	14	gp35 WITH protein	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/12/09 19:42
-	5	(US-5877279-$ or US-6437112-$ or US-5864013-$).did. or (WO-9611947-$).did. or (WO-200077196-$).did.	USPAT; EPO; DERWENT	2003/12/09 19:41
-	4	gp35 WITH isolated	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/12/09 19:42
-	6	gp35 WITH purified	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/12/09 19:42

(FILE 'HOME' ENTERED AT 14:18:19 ON 09 DEC 2003)

FILE 'MEDLINE, AGRICOLA, CANCERLIT, SCISEARCH, CAPLUS, MEDICONF' ENTERED AT 14:18:41 ON 09 DEC 2003

L1 89436 S BACTERIOPHAGE
L2 173 S L1 AND (T4 TAIL)
L3 117 DUP REM L2 (56 DUPLICATES REMOVED)
L4 4 S L3 AND (GP35 OR P35)
L5 6 S L2 AND (GP35 OR P35)
L6 5 DUP REM L5 (1 DUPLICATE REMOVED)

FILE 'STNGUIDE' ENTERED AT 14:27:30 ON 09 DEC 2003

FILE 'MEDLINE, AGRICOLA, CANCERLIT, SCISEARCH, CAPLUS, MEDICONF' ENTERED AT 14:28:56 ON 09 DEC 2003

L7 24 S L1 AND (GP35 OR P35)
L8 17 DUP REM L7 (7 DUPLICATES REMOVED)
L9 17 SORT L8 PY

=> d an ti so au ab pi l9 2 3 4 5 10 13 16

L9 ANSWER 2 OF 17 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1973:544087 CAPLUS
DN 79:144087
TI Assembly of **Bacteriophage** T4 tail fibers. IV. Subunit composition of tail fibers and fiber precursors
SO Journal of Molecular Biology (1973), 79(4), 633-47
CODEN: JMOBAK; ISSN: 0022-2836
AU Dickson, Robert C.
AB Using a novel purifn. procedure, the protein compn. of the tail fibers of **bacteriophage** T4 has been detd. Fibers contain 4 proteins whose mol. wts. as estd. by Na dodecyl sulfate-acrylamide gel electrophoresis, are 150,000; 125,000; 40,000; and 24,000. The 2 largest proteins have been previously identified as the products of genes 34 (P34) and 37(P37), resp. The 2 smaller proteins have now been identified as the products of genes 35 (**P35**) and 36 (P36), resp. The products of the 2 other known phage genes required for fiber assembly, 38 and 57, have been identified as nonstructural phage proteins with mol. wts. of 26,000 and 10,000 resp.

L9 ANSWER 3 OF 17 MEDLINE on STN
AN 82127583 MEDLINE
TI Organization of the **bacteriophage** T4 tail fiber gene cluster 34-38.
SO PROGRESS IN CLINICAL AND BIOLOGICAL RESEARCH, (1981) 64 353-64.
Journal code: 7605701. ISSN: 0361-7742.
AU Revel H R
AB A correlation of the genetic, functional, and structural maps of the T4 tail fiber gene cluster has been achieved by analysis of lambda derivatives carrying genes 34-38. 31 recombinants carrying different parts of the T4 tail fiber gene cluster were identified by a marker rescue screen of 300 lambda T4 recombinant clones, generated by restriction of partial cytosine-containing T4 DNA with E coRI or with HindIII and ligation into appropriately cleaved lambda replacement vectors. Extensive genetic characterization revealed 15 recombinant classes with respect to the contiguous stretches of genome recovered and suggested the presence of 7 HindIII sites and 8 EcoRI sites in the 10 kb region. Functional analysis showed tht genes 34-38 were recovered intact. The tail fiber genes are efficiently expressed from lambda promoters and complement T4 amber mutants in a modified in vivo complementation test. Polypeptides, Mr = 145,000, 105,000, 39,000, 27,000 and 24,000 corresponding to gp34, gp37, **gp35**, gp38 and gp36 respectively, were detected by SDS polyacrylamide gel electrophoresis of 35S- labeled extracts of lambda T4 recombinant infected UV-treated host cells. Restriction enzyme structural analysis of the lambda T4 DNAs identified 7 HindIII and 7 EcoRI fragments and established a restriction map covering about 11 kb. The correlation of the genetic, functional and restriction maps provides a rational approach to a genetically directed DNA sequence analysis of the T4 tail fiber genes and of their mutant variants which affect particular aspects of tail fiber assembly, structure and function.

L9 ANSWER 4 OF 17 MEDLINE on STN
AN 96326707 MEDLINE
TI Stoichiometry and domainal organization of the long tail-fiber of **bacteriophage** T4: a hinged viral adhesin.
SO JOURNAL OF MOLECULAR BIOLOGY, (1996 Aug 2) 260 (5) 767-80.
Journal code: 2985088R. ISSN: 0022-2836.
AU Cerritelli M E; Wall J S; Simon M N; Conway J F; Steven A C
AB The long-tail fibers (LTFs) form part of **bacteriophage** T4's apparatus for host cell recognition and infection, being responsible for its initial attachment to susceptible bacteria. The LTF has two parts, each approximately 70 to 75 nm long; gp34 (140 kDa) forms the proximal half-fiber, while the distal half-fiber is composed of gp37 (109 kDa), gp36(23 kDa) and **gp35** (30 kDa). LTFs have long been thought to be dimers of gp34, gp37 and gp36, with one copy of **gp35**. We have used mass mapping by scanning transmission electron microscopy (STEM), quantitative SDS-PAGE, and computational sequence analysis to study the structures of purified LTFs and half-fibers of both kinds. These data establish that the LTF is, in fact, trimeric, with a stoichiometry of gp34: gp37: gp36: **gp35** = 3:3:3:1. Averaged images of stained and unstained molecules resolve the LTF into a linear stack of 17 domains. At the proximal end is a globular domain of approximately 145 kDa that becomes incorporated into the baseplate. It is followed by a rod-like shaft (33 x 4 mm; 151 kDa) which correlates with a cluster of seven quasi repeats, each 34 to 39 residues long. The proximal half-fiber terminates in three globular domains. The distal half-fiber consists of ten globular domains of variable size and spacing, preceding a needle-like end domain (15 x 2.5 nm; 31 kDa). The LTF is rigid apart from hinges between the two most proximal domains, and between the proximal and distal half-fibers. The latter hinge occurs at a site of local non-equivalence (the "kneecap") at which density, correlated with the presence of **gp35**, bulges asymmetrically out on one side. Several observations indicate that gp34 participates in the sharing of conserved structural modules among coliphage tail-fiber genes to which gp37 was previously noted to subscribe. Two adjacent globular domains in the proximal half-fiber match a pair of domains in the distal half-fiber, and the rod domain in the proximal half-fiber resembles a similar domain in the T4 short tail-fiber (gp12). Finally, possible structures are considered; combining our data with earlier observations, the most likely conformation for most of the LTF is a three-stranded beta-helix.

L9 ANSWER 5 OF 17 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1996:404766 CAPLUS
DN 125:51926
TI Tail fiber proteins of T-even-like **bacteriophage** for the production of nanometer structures and use thereof
SO PCT Int. Appl., 82 pp.
CODEN: PIXXD2
IN Goldberg, Edward B.
AB Described is the prepn. of nanostructures, i.e., nanometer sized structures useful in the construction of microscopic and macroscopic structures, based on **bacteriophage** T4 tail fiber proteins and variants thereof. Prepn. of single or fusion proteins or their variants selected from gp34, **gp35**, gp36, and gp37 of T-4 **bacteriophage** was demonstrated. Also provided are kits for making nanostructures, comprising purified, e.g., **gp35** and gp36-34 chimer, or gp37-36 chimer.

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9611947	A1	19960425	WO 1995-US13023	19951013
W: AL, AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, UZ, VN				
RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 5877279	A	19990302	US 1994-322760	19941013
CA 2202474	AA	19960425	CA 1995-2202474	19951013
AU 9538296	A1	19960506	AU 1995-38296	19951013
AU 689662	B2	19980402		

EP 785946		A1	19970730	EP 1995-936297	19951013
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE					
BR 9509487		A	19970930	BR 1995-9487	19951013
CN 1168676		A	19971224	CN 1995-196597	19951013
CN 1113068		B	20030702		
HU 77683		A2	19980728	HU 1998-746	19951013
JP 10508194		T2	19980818	JP 1996-513358	19951013
RU 2162856		C2	20010210	RU 1997-107477	19951013

L9 ANSWER 10 OF 17 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:69916 CAPLUS
DN 130:135644
TI Use of **bacteriophage** T4 tail fiber proteins in the preparation of nanostructures
SO U.S., 51 pp., Cont.-in-part of U.S. Ser. No. 322,760.
CODEN: USXXAM
IN Goldberg, Edward B.
AB Methods of using the gp34, **gp35**, gp36, and gp37 tail fiber proteins of **bacteriophage** T4 in the formation of nanostructures that can be used in nanomachines is described. In particular, variants of the proteins that show altered patterns of interaction, thermolability of interaction, or geometry of interaction can be used to create an array of self-assembling structures.

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 5864013	A	19990126	US 1995-542003	19951012
US 5877279	A	19990302	US 1994-322760	19941013
CA 2202474	AA	19960425	CA 1995-2202474	19951013
CN 1168676	A	19971224	CN 1995-196597	19951013
CN 1113068	B	20030702		
HU 77683	A2	19980728	HU 1998-746	19951013
US 6437112	B1	20020820	US 1999-236949	19990125

L9 ANSWER 13 OF 17 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2000:900798 CAPLUS
DN 134:67178
TI Cloning and characterization of phage T4 gene **gp35**
SO PCT Int. Appl., 75 pp.
CODEN: PIXXD2
IN Goldberg, Edward B.
AB The invention provides sequences of phage T4 gene **gp35** and its encoded protein and cDNA sequences of a novel human gene which is located between gene gp34 and gene gp36. Gene **gp35** encodes a tail fiber protein which functions to join the rodlike proximal and distal halves of the **bacteriophage** tail fibers. A thermostable **gp35** mutant protein is also isolated from a ts mutant. The present invention further relates to the use of **bacteriophage** T4 **gp35** gene and protein products as well as derivs., variants, and analogs thereof in the construction of nanostructures.

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000077196	A1	20001221	WO 1999-US13024	19990611
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9946781	A1	20010102	AU 1999-46781	19990611
EP 1185638	A1	20020313	EP 1999-930192	19990611
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2003507007	T2	20030225	JP 2001-503640	19990611

L9 ANSWER 16 OF 17 MEDLINE on STN
AN 2003285755 MEDLINE
TI Identification and mutational analysis of **bacteriophage** PRD1

holin protein **P35**.

SO JOURNAL OF BACTERIOLOGY, (2003 Jul) 185 (13) 3795-803.
Journal code: 2985120R. ISSN: 0021-9193.

AU Rydman Pia S; Bamford Dennis H

AB Holin proteins are phage-induced integral membrane proteins which regulate the access of lytic enzymes to host cell peptidoglycan at the time of release of progeny viruses by host cell lysis. We describe the identification of the membrane-containing phage PRD1 holin gene (gene XXXV). The PRD1 holin protein (**P35**, 12.8 kDa) acts similarly to its functional counterpart from phage lambda (gene S), and the defect in PRD1 gene XXXV can be corrected by the presence of gene S of lambda. Several nonsense, missense, and insertion mutations in PRD1 gene XXXV were analyzed. These studies support the overall conclusion that the charged amino acids at the protein C terminus are involved in the timing of host cell lysis.